

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/938,294

DATE: 09/10/2001

TIME: 08:51:11

Input Set : A:\16517.253filedsequence listing.txt

Output Set: N:\CRF3\09102001\I938294.raw

ENTERED

1 <110> APPLICANT: Gregory J. Hinkle  
 2 Jingdong Liu  
 3 Linda T. Parker  
 5 <120> TITLE OF INVENTION: Novel Plant Transcribed Regions and Uses Thereof  
 7 <130> FILE REFERENCE: 38-21(51952)B/16517.253  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/938,294 OK  
 C--> 9 <141> CURRENT FILING DATE: 2001-08-24  
 9 <150> PRIOR APPLICATION NUMBER: 60/228,466  
 10 <151> PRIOR FILING DATE: 2000-08-29  
 12 <160> NUMBER OF SEQ ID NOS: 86  
 14 <210> SEQ ID NO: 1  
 15 <211> LENGTH: 463  
 16 <212> TYPE: DNA  
 17 <213> ORGANISM: Zea mays  
 19 <220> FEATURE:  
 20 <221> NAME/KEY: CDS  
 21 <222> LOCATION: (52)..(240)  
 23 <400> SEQUENCE: 1  
 25 ccacgcgtcc gcaacaattt gatcaggcaa taacctgacg accctgggtt g ttc tgt 57  
 26 Phe Cys  
 27 1  
 29 gaa tgc att ttc gtc gtg ctt caa caa cag gga ccg gac tac atg gtc 105  
 30 Glu Cys Ile Phe Val Val Leu Gln Gln Gly Pro Asp Tyr Met Val  
 31 5 10 15  
 33 cgc aac gca agg agg tcc atg ctg gag gag ctg gag ggg atg ctg gag 153  
 34 Arg Asn Ala Arg Arg Ser Met Leu Glu Glu Leu Glu Gly Met Leu Glu  
 35 20 25 30  
 37 atc gtg gag cct cag ccg ccg ggg aag ccg agg acg ctt agc cgc agg 201  
 38 Ile Val Glu Pro Gln Pro Pro Gly Lys Pro Arg Thr Leu Ser Arg Arg  
 39 35 40 45 50  
 41 agg ttc gat ctg cca gaa ggc gta gcc atc gaa aag gag acgcgggagg 250  
 42 Arg Phe Asp Leu Pro Glu Gly Val Ala Ile Glu Lys Glu  
 43 55 60  
 45 cgggcaagtg aagtgcacg gtgggtggtg gcatgcttg gcatgttggt atatgocga 310  
 47 tgcggactat agagtttgag tttgtgctgc taccgaaccg tggaccacct taccocgttg 370  
 49 agatgtttga tagctggact tttgtgctg ttgtatttgt agaccagaac gttgttcttt 430  
 51 gtaataaatt ggcgtgtgct gctttttgct aat 463  
 54 <210> SEQ ID NO: 2  
 55 <211> LENGTH: 1702  
 56 <212> TYPE: DNA  
 57 <213> ORGANISM: Zea mays  
 59 <220> FEATURE:  
 60 <221> NAME/KEY: CDS  
 61 <222> LOCATION: (63)..(1484)  
 63 <400> SEQUENCE: 2  
 65 attcggctcg agttgatcc gagccacag tctctcctcg ggccaccgc gtccgaccgg 60  
 67 cg atg gca aag acc ccg tgc ttc gcg gtg gcg gcg gtc gcc gga ggc 107

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68   Met Ala Lys Thr Pro Ser Phe Ala Val Ala Ala Val Ala Gly Gly
69   1           5           10          15
71   cgc ggg ccg gtt cac aac cgg acc cag ctc ctc ctc ctc ctc ctc gtg      155
72   Arg Gly Pro Val His Asn Arg Thr Gln Leu Leu Leu Leu Leu Leu Val
73           20           25           30
75   gcc gtc gca gcc tcc gca tcc aca gca ggg ttc ctc ctc cgc ggt gcc      203
76   Ala Val Ala Ala Ser Ala Ser Thr Ala Gly Phe Leu Leu Arg Gly Ala
77           35           40           45
79   ctg cga gac cct tgc gac ggc cgt ggg gac ccc gcc gcc ctc aac acc      251
80   Leu Arg Asp Pro Cys Asp Gly Arg Gly Asp Pro Ala Ala Leu Asn Thr
81           50           55           60
83   gcc gtc gcc agc ggg agt ccc ctc ggg ttc atg agg tcc aag ctc gtg      299
84   Ala Val Ala Ser Gly Ser Pro Leu Gly Phe Met Arg Ser Lys Leu Val
85           65           70           75
87   ctc ctc gtc tcc cat gag ctc tcc ctc tct ggt ggt cca ctt tta ctg      347
88   Leu Leu Val Ser His Glu Leu Ser Leu Ser Gly Gly Pro Leu Leu Leu
89   80           85           90           95
91   atg gaa tta gca ttt ctt ctg agg cat gtt ggc tcg caa gtg gtg tgg      395
92   Met Glu Leu Ala Phe Leu Leu Arg His Val Gly Ser Gln Val Val Trp
93           100          105          110
95   ata aca aac cag aga tca caa gaa aca aat gat gtc aca tat agc ttg      443
96   Ile Thr Asn Gln Arg Ser Gln Glu Thr Asn Asp Val Thr Tyr Ser Leu
97           115          120          125
99   gag cat agg atg ttg aac cat gga gtg cag gtt tta cca gct aga gga      491
100  Glu His Arg Met Leu Asn His Gly Val Gln Val Leu Pro Ala Arg Gly
101           130          135          140
103  cag gag gca gtt gat att gct cta aaa gct gat ctg gtt atc tta aac      539
104  Gln Glu Ala Val Asp Ile Ala Leu Lys Ala Asp Leu Val Ile Leu Asn
105           145          150          155
107  act gct gtt gct ggc aag tgg ctt gac cct gtt ctg aaa gat cat gtt      587
108  Thr Ala Val Ala Gly Lys Trp Leu Asp Pro Val Leu Lys Asp His Val
109  160           165          170          175
111  cct aaa gtc ctt ccg aag att ttg tgg tgg atc cat gaa atg cgt ggg      635
112  Pro Lys Val Leu Pro Lys Ile Leu Trp Trp Ile His Glu Met Arg Gly
113           180          185          190
115  cat tac ttt aag gtt gaa tat gtc aaa cat ott ccc ttt gtt gct gga      683
116  His Tyr Phe Lys Val Glu Tyr Val Lys His Leu Pro Phe Val Ala Gly
117           195          200          205
119  gcc atg att gat tct cat aca acg gct gag tat tgg aat agc agg act      731
120  Ala Met Ile Asp Ser His Thr Thr Ala Glu Tyr Trp Asn Ser Arg Thr
121           210          215          220
123  agc gat cgc ctg aaa ata cag atg cca caa act tat gtt gtt cac ctg      779
124  Ser Asp Arg Leu Lys Ile Gln Met Pro Gln Thr Tyr Val Val His Leu
125           225          230          235
127  ggg aat agt aaa gaa cta atg gaa gtt gct gaa gac aat gtc gca aga      827
128  Gly Asn Ser Lys Glu Leu Met Glu Val Ala Glu Asp Asn Val Ala Arg
129  240           245          250          255
131  aga gtc cta cgg gaa cat att cgt gaa tcc ctt gga gta cgg agt gag      875
132  Arg Val Leu Arg Glu His Ile Arg Glu Ser Leu Gly Val Arg Ser Glu

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133          260          265          270
135 gat ctc ctg ttt gca ata ata aac agt gta tca cga gga aag gga caa      923
136 Asp Leu Leu Phe Ala Ile Ile Asn Ser Val Ser Arg Gly Lys Gly Gln
137          275          280          285
139 gac tta ttt ctt caa gca ttt tat cag gct ttg cag ctc atc caa cac      971
140 Asp Leu Phe Leu Gln Ala Phe Tyr Gln Ala Leu Gln Leu Ile Gln His
141          290          295          300
143 gag aaa ctt aaa gtg cct aga ata cat gct gta gtt gtg gga agt gat      1019
144 Glu Lys Leu Lys Val Pro Arg Ile His Ala Val Val Val Gly Ser Asp
145          305          310          315
147 gtt aat gct cag acc aaa ttt gag act cag tta cgt gac ttt gtg gtg      1067
148 Val Asn Ala Gln Thr Lys Phe Glu Thr Gln Leu Arg Asp Phe Val Val
149 320          325          330          335
151 aag aac acg att cat gac cgt gtc cat ttt gtg aac aag aca ttg gca      1115
152 Lys Asn Thr Ile His Asp Arg Val His Phe Val Asn Lys Thr Leu Ala
153          340          345          350
155 gtg gcc cct tac ttg gca gca att gat gtg ctt gtt cag aat tct cag      1163
156 Val Ala Pro Tyr Leu Ala Ala Ile Asp Val Leu Val Gln Asn Ser Gln
157          355          360          365
159 ggc cgt gga gaa tgc ttt gga agg ata aca att gaa gca atg gca ttc      1211
160 Gly Arg Gly Glu Cys Phe Gly Arg Ile Thr Ile Glu Ala Met Ala Phe
161          370          375          380
163 aag ttg cca gta ttg ggc acg gct gct gga ggg acc acg gag atc gtc      1259
164 Lys Leu Pro Val Leu Gly Thr Ala Ala Gly Gly Thr Thr Glu Ile Val
165          385          390          395
167 ctg gac ggc tcg act ggc ctt ctg cat cct gct ggg aag gag ggc gtg      1307
168 Leu Asp Gly Ser Thr Gly Leu Leu His Pro Ala Gly Lys Glu Gly Val
169 400          405          410          415
171 gcg cct ctt gca aag aac atc gtc aga ctc gca agc cac gcc gag cag      1355
172 Ala Pro Leu Ala Lys Asn Ile Val Arg Leu Ala Ser His Ala Glu Gln
173          420          425          430
175 agg gtc tcc atg ggg gaa aag ggc tat ggc agg gtg aag gaa atg ttc      1403
176 Arg Val Ser Met Gly Glu Lys Gly Tyr Gly Arg Val Lys Glu Met Phe
177          435          440          445
179 atg gag cac cac atg gct gag agg atc gcg gcg gtg ttg aag gat gtc      1451
180 Met Glu His His Met Ala Glu Arg Ile Ala Ala Val Leu Lys Asp Val
181          450          455          460
183 ctg agg aaa tca cag gag cac tcc agg tct tga gctttgccgt gcccatcagc      1504
184 Leu Arg Lys Ser Gln Glu His Ser Arg Ser
185          465          470
187 ttgcgctaac atgttgaact agattttacg ggctacgcct acgtggttca ggctgtaaac      1564
189 tgtagattgc actctgttg tctacttttt cacattcatg ttttacctat taggccatgt      1624
191 ccgattctat tccaattcat ataggttcta tttcaatcca tatagattaa gagggattga      1684
193 ggagatttca atcttagt      1702
196 <210> SEQ ID NO: 3
197 <211> LENGTH: 1430
198 <212> TYPE: DNA
199 <213> ORGANISM: Zea mays
201 <220> FEATURE:

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202 <221> NAME/KEY: CDS
203 <222> LOCATION: (1)..(1203)
205 <400> SEQUENCE: 3
207 cca cgc gtc cgt cta att ata gaa aag aat aga gac tac aca gtt gat      48
208 Pro Arg Val Arg Leu Ile Ile Glu Lys Asn Arg Asp Tyr Thr Val Asp
209 1          5          10          15
211 tat agc agc tca tct ttt gga cta tca ggt gct agt tat ata tca tcc      96
212 Tyr Ser Ser Ser Ser Phe Gly Leu Ser Gly Ala Ser Tyr Ile Ser Ser
213          20          25          30
215 ccc atg agg gaa aca gag cag tca aag act agt ttt gac cag ttt tat      144
216 Pro Met Arg Glu Thr Glu Gln Ser Lys Thr Ser Phe Asp Gln Phe Tyr
217          35          40          45
219 tct aat gcc aat ttc cag ttg tat ttg tcc ttc tgc aac ttt gac aag      192
220 Ser Asn Ala Asn Phe Gln Leu Tyr Leu Ser Phe Cys Asn Phe Asp Lys
221          50          55          60
223 gca atg ttc ttg ggt ttc ttt cat gag cta tcc gag ctt ccc ttt gaa      240
224 Ala Met Phe Leu Gly Phe Phe His Glu Leu Ser Glu Leu Pro Phe Glu
225 65          70          75          80
227 ctg caa aga aaa gct gtc aga gat ttg aag act tct ctg agc ggt gaa      288
228 Leu Gln Arg Lys Ala Val Arg Asp Leu Lys Thr Ser Leu Ser Gly Glu
229          85          90          95
231 aat gaa att tgg cat tct atg gtc tac aat ggg ttt ttt gaa gca ttc      336
232 Asn Glu Ile Trp His Ser Met Val Tyr Asn Gly Phe Phe Glu Ala Phe
233          100          105          110
235 cat gaa ttc ctc aag aat gac agt gga att cac aca ctg caa gct cga      384
236 His Glu Phe Leu Lys Asn Asp Ser Gly Ile His Thr Leu Gln Ala Arg
237          115          120          125
239 agg gct ggg att cag ttt ttt ctt gct ttc ctt tct agt ggc agg gct      432
240 Arg Ala Gly Ile Gln Phe Phe Leu Ala Phe Leu Ser Ser Gly Arg Ala
241          130          135          140
243 cga att cct tca gtt tgt gaa gat gtg gta ctt ctg att gca tca cta      480
244 Arg Ile Pro Ser Val Cys Glu Asp Val Val Leu Leu Ile Ala Ser Leu
245 145          150          155          160
247 cat gat tcc gag ttc aaa cag gag gct ctt ctg att gta cat gaa ctg      528
248 His Asp Ser Glu Phe Lys Gln Glu Ala Leu Leu Ile Val His Glu Leu
249          165          170          175
251 ctt cag gaa cca agc tgt cca aaa tct agt ctc atg gcc tcc att ctt      576
252 Leu Gln Glu Pro Ser Cys Pro Lys Ser Ser Leu Met Ala Ser Ile Leu
253          180          185          190
255 tct cct tca gtg ttt gga gct ttg gac agt gga gaa acc aag tgc ctg      624
256 Ser Pro Ser Val Phe Gly Ala Leu Asp Ser Gly Glu Thr Lys Cys Leu
257          195          200          205
259 gac ctc gct ctg cag atc atc tgc aag att tca tct gat aat gat ata      672
260 Asp Leu Ala Leu Gln Ile Ile Cys Lys Ile Ser Ser Asp Asn Asp Ile
261          210          215          220
263 aaa tct tac ctt ctt tcg tcc gga ata gtg tcg agg tta tct ccg ctc      720
264 Lys Ser Tyr Leu Leu Ser Ser Gly Ile Val Ser Arg Leu Ser Pro Leu
265 225          230          235          240
267 ctt ggt gaa gga aag atg aca gaa tgc tct ttg aag att cta cgg aac      768

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268 Leu Gly Glu Gly Lys Met Thr Glu Cys Ser Leu Lys Ile Leu Arg Asn
269                245                250                255
271 ttg agt gac gtg aaa gag acc gca ggg ttt ata atc aga aca ggt aat      816
272 Leu Ser Asp Val Lys Glu Thr Ala Gly Phe Ile Ile Arg Thr Gly Asn
273                260                265                270
275 tgc gtc agc tcc att tca gat cat ctg gac act gga agc cac agc gaa      864
276 Cys Val Ser Ser Ile Ser Asp His Leu Asp Thr Gly Ser His Ser Glu
277                275                280                285
279 cgt gaa cat gcg gtg gtc atc ctt cta ggg gta tgc tcc cac agt cct      912
280 Arg Glu His Ala Val Val Ile Leu Leu Gly Val Cys Ser His Ser Pro
281                290                295                300
283 gag gtt tgt tca ctt tcc atg aag gaa ggc gtc atc cca gcc ctt gta      960
284 Glu Val Cys Ser Leu Ser Met Lys Glu Gly Val Ile Pro Ala Leu Val
285 305                310                315                320
287 gac tta tca gtg agt gga acc aag gtg gca agg gat tgc tcg gtc aag      1008
288 Asp Leu Ser Val Ser Gly Thr Lys Val Ala Arg Asp Cys Ser Val Lys
289                325                330                335
291 ttg ctt cag ctt ctg agg aac ttc agg cga tgt gac cag ttc agc agt      1056
292 Leu Leu Gln Leu Leu Arg Asn Phe Arg Arg Cys Asp Gln Phe Ser Ser
293                340                345                350
295 tca tgc tca aga gag ctt gct gtc gat cat gtt tca gag aac act cgc      1104
296 Ser Cys Ser Arg Glu Leu Ala Val Asp His Val Ser Glu Asn Thr Arg
297                355                360                365
299 aat ggt tca att tgc atg cag ccg ata tca aag tca gcc cgg tat att      1152
300 Asn Gly Ser Ile Cys Met Gln Pro Ile Ser Lys Ser Ala Arg Tyr Ile
301                370                375                380
303 tca aga aag ctc aac ctt ttc tca aaa cct cgg tcg ctg acc ctg gct      1200
304 Ser Arg Lys Leu Asn Leu Phe Ser Lys Pro Arg Ser Leu Thr Leu Ala
305 385                390                395                400
307 tga gaaatggaag gggtcggttg gatcgagccc tattccgcag cgctaactgc      1253
309 cagatgtaca gatagtagca ggtagcgttc gtcgagatga aatgtttgtg ggaggctttt      1313
311 taaaactcac catgtatttc aagagttttt attagttttt tttggatttt ctttactggc      1373
313 gctacaaaca gtagatgtat gactgttcga gctggaaacc tgtgcgcttt ttatcgt      1430
316 <210> SEQ ID NO: 4
317 <211> LENGTH: 1048
318 <212> TYPE: DNA
319 <213> ORGANISM: Zea mays
321 <220> FEATURE:
322 <221> NAME/KEY: CDS
323 <222> LOCATION: (129)..(578)
325 <400> SEQUENCE: 4
327 ccacgcgtcc gtcacagcgt tgagccaact ccgcccacct gtcgttttcg cctctcccta      60
329 gcattttaccg gaagaaacga gcgtgaccgc cgcctttctcc cgtcccgct cccgctctgc      120
331 atctctcc atg ggc cag atc gag agc cag gtc act cct cca gcg gag gag      170
332      Met Gly Gln Ile Glu Ser Gln Val Thr Pro Pro Ala Glu Glu
333      1                5                10
335 cct tct cca ccc acc gtg gag ccg tcg ccg tcg tct cct gcc ccg cct      218
336 Pro Ser Pro Pro Thr Val Glu Pro Ser Pro Ser Ser Pro Ala Pro Pro
337 15                20                25                30

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/938,294

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Input Set : A:\16517.253filedsequence listing.txt

Output Set: N:\CRF3\09102001\I938294.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date